

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 23, 2005, 11:45:50 ; Search time 6433 Seconds
(without alignments)
10801.303 Million cell updates/sec

Title: US-10-790-224A-19
Perfect score: 1434
Sequence: 1 gtggcggtttgaaaccccgga.....aattgtacttcgactgctaa 1434

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					
Result		Query					
No.	Score	Match	Length	DB	ID	Description	
1	1434	100.0	1434	6	CQ871075	CQ871075 Sequence	
2	1434	100.0	2500	6	CQ817721	CQ817721 Sequence	
3	1424.4	99.3	1554	6	AX063815	AX063815 Sequence	

	4	1424.4	99.3	3686	1	CGGLNA	Y13221 Corynebacte
	5	1424.4	99.3	326150	1	AP005281	AP005281 Corynebac
	6	1424.4	99.3	349575	1	BX927154	BX927154 Corynebac
	7	1424.4	99.3	349980	6	AX127150	AX127150 Sequence
	8	1421.4	99.1	1431	6	BD165686	BD165686 Novel pol
	9	1421.4	99.1	1431	6	AX123569	AX123569 Sequence
	10	1397.2	97.4	1690	1	AF005635	AF005635 Corynebac
	11	1098.6	76.6	306650	1	AP005221	AP005221 Corynebac
	12	936.2	65.3	348408	1	BX248358	BX248358 Corynebac
c	13	816.2	56.9	110000	1	AP006618_18	Continuation (19 o
	14	784.2	54.7	2216	1	AY008693	AY008693 Mycobacte
	15	752.8	52.5	313846	1	AE017234	AE017234 Mycobacte
	16	705.8	49.2	1437	1	AF458290	AF458290 Mycobacte
	17	705.8	49.2	1437	6	AX935596	AX935596 Sequence
	18	705.8	49.2	1872	1	MTU87280	U87280 Mycobacteri
	19	705.8	49.2	38793	1	MSG827CS	L78817 Mycobacteri
	20	705.8	49.2	110000	1	AE000516_24	Continuation (25 o
	21	705.8	49.2	306050	1	BX248341	BX248341 Mycobacte
	22	705.8	49.2	348247	1	BX842579	BX842579 Mycobacte
	23	705.8	49.2	348450	1	MLEPRTN4	AL583920 Mycobacte
	24	704.2	49.1	1437	6	AR361070	AR361070 Sequence
	25	704.2	49.1	1437	6	BD064140	BD064140 Abundant
	26	693.2	48.3	12641	1	AE014731	AE014731 Bifidobac
	27	693.2	48.3	349980	6	AX492785	AX492785 Sequence
	28	693.2	48.3	349980	6	AX553952	AX553952 Sequence
	29	673.2	46.9	2280	1	STMGLNA	M23172 Streptomyce
	30	673.2	46.9	321250	1	SCO939111	AL939111 Streptomy
	31	665.8	46.4	2600	1	AF050112	AF050112 Amycolato
c	32	663.2	46.2	299925	1	AP005045	AP005045 Streptomy
	33	661.6	46.1	1889	1	SRU58138	U58138 Streptomyce
c	34	658.4	45.9	110000	1	AE016822_10	Continuation (11 o
	35	654	45.6	1410	1	SVGLNAIA	X70924 S.viridochr
	36	581.6	40.6	34088	6	CQ363778	CQ363778 Sequence
c	37	581.6	40.6	110000	1	AE017283_07	Continuation (8 of
	38	578.4	40.3	1719	1	FRAGLNAA	L10631 Frankia aln
c	39	538.8	37.6	110000	1	AE017180_19	Continuation (20 o
c	40	538.8	37.6	110000	1	AE017180_20	Continuation (21 o
	41	533.8	37.2	299700	1	AP006571	AP006571 Gloeobact
c	42	524.4	36.6	197050	1	AL646081	AL646081 Ralstonia
	43	492.6	34.4	1910	1	AZSGLN	M26107 A.brasilens
	44	492.4	34.3	300600	1	AP005952	AP005952 Bradyrhiz
	45	490.2	34.2	1950	1	AVIGLNA	M57275 A.vinelandi

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 23, 2005, 08:55:40 ; Search time 840 Seconds
(without alignments)
10105.844 Million cell updates/sec

Title: US-10-790-224A-19
Perfect score: 1434
Sequence: 1 gtggcgtttgaaaccccgga.....aattgtacttcgactgctaa 1434

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1434	100.0	1434	13	ADS73713	Ads73713 B. lactof
2	1434	100.0	2500	12	ADP87711	Adp87711 Brevibact
3	1424.4	99.3	1554	4	AAF71801	Aaf71801 Corynebact
4	1424.4	99.3	349980	5	AAH68531	Aah68531 C.glutami

	5	1421.4	99.1	1431	5	AAH68450	Aah68450 C glutami
	6	933.2	65.1	1434	8	ACA29721	Aca29721 Prokaryot
	7	705.8	49.2	1437	2	AAV42598	Aav42598 M. tuberc
	8	705.8	49.2	1437	2	AAV29069	Aav29069 Mycobacte
	9	705.8	49.2	1437	10	ADF18437	Adf18437 Mycobacte
	10	705.8	49.2	38110	8	AAL53730	Aal53730 Ribonucle
	11	705.8	49.2	38110	8	AAD49662	Aad49662 Mycobacte
	12	705.8	49.2	110000	4	AAI99682_24	Continuation (25 o
	13	705.8	49.2	110000	4	AAI99683_24	Continuation (25 o
	14	704.2	49.1	1437	2	AAT71594	Aat71594 Mycobacte
	15	704.2	49.1	1437	10	AAD59703	Aad59703 M. tuberc
	16	693.2	48.3	349980	6	ABQ81847	Abq81847 Bifidobac
	17	581.6	40.6	34088	4	AAS59566	Aas59566 Propionib
	18	581.6	40.6	34088	8	ACF64495	Acf64495 Propionib
	19	483.8	33.7	1410	4	AAS54353	Aas54353 Pseudomon
	20	483.8	33.7	1410	8	ACA42733	Aca42733 Prokaryot
	21	481	33.5	1446	11	ABD17636	Abd17636 Pseudomon
c	22	479.6	33.4	1500	11	ABD17747	Abd17747 Pseudomon
	23	460.2	32.1	1497	8	ACA27260	Aca27260 Prokaryot
	24	458.8	32.0	1404	8	ACA43893	Aca43893 Prokaryot
	25	456	31.8	1413	8	ACA23419	Aca23419 Prokaryot
	26	449.6	31.4	1413	8	ACA25929	Aca25929 Prokaryot
	27	446.2	31.1	1407	8	ACA31947	Aca31947 Prokaryot
	28	434.8	30.3	1404	8	ACA45511	Aca45511 Prokaryot
	29	423.6	29.5	1410	8	ACA53509	Aca53509 Prokaryot
	30	419	29.2	1407	8	ACA35419	Aca35419 Prokaryot
	31	415.2	29.0	1431	11	ACH99251	Ach99251 Klebsiell
c	32	415.2	29.0	1488	11	ACH99262	Ach99262 Klebsiell
	33	398	27.8	1410	8	ACA53962	Aca53962 Prokaryot
	34	392	27.3	1344	8	ACA25130	Aca25130 Prokaryot
	35	391.8	27.3	1410	4	AAS52684	Aas52684 E. coli D
	36	391.8	27.3	1410	8	ACA32714	Aca32714 Prokaryot
	37	391.8	27.3	1410	10	ADI53076	Adi53076 E. coli g
	38	391.8	27.3	1410	12	ADI38943	Adi38943 Glutamine
	39	391.2	27.3	1410	4	AAS56054	Aas56054 Salmonell
	40	391.2	27.3	1410	8	ACA52006	Aca52006 Prokaryot
	41	382.2	26.7	1419	8	ACA42021	Aca42021 Prokaryot
c	42	375.8	26.2	1530	10	ABZ41832	Abz41832 N. gonorr
	43	375	26.2	1409	8	ACA49431	Aca49431 Prokaryot
	44	374.8	26.1	1533	8	ACA41116	Aca41116 Prokaryot
	45	374.8	26.1	1572	10	ABZ41834	Abz41834 N. gonorr

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 23, 2005, 10:08:30 ; Search time 269 Seconds
(without alignments)
8722.754 Million cell updates/sec

Title: US-10-790-224A-19
Perfect score: 1434
Sequence: 1 gtggcggtttgaaaccccgga.....aattgtacttcgactgctaa 1434

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query				Description
	No.	Score	Match	Length	DB	ID			
	1	705.8	49.2	1437	3	US-08-724-814-15			Sequence 15, Appl
	2	705.8	49.2	4403765	3	US-09-103-840A-2			Sequence 2, Appli
	3	705.8	49.2	4411529	3	US-09-103-840A-1			Sequence 1, Appli
	4	704.2	49.1	1437	4	US-09-157-689-93			Sequence 93, Appl
	5	481	33.5	1446	4	US-09-252-991A-16240			Sequence 16240, A
c	6	479.6	33.4	1500	4	US-09-252-991A-16351			Sequence 16351, A
	7	415.2	29.0	1431	4	US-09-489-039A-5046			Sequence 5046, Ap
c	8	415.2	29.0	1488	4	US-09-489-039A-5057			Sequence 5057, Ap
	9	335	23.4	1470	4	US-09-328-352-237			Sequence 237, App
	10	328.6	22.9	948	4	US-09-252-991A-16139			Sequence 16139, A
	11	289	20.2	1482	4	US-09-543-681A-2582			Sequence 2582, Ap

	12	277.6	19.4	1830121	4	US-09-557-884-1	Sequence 1, Appli
	13	277.6	19.4	1830121	4	US-09-643-990A-1	Sequence 1, Appli
	14	247.4	17.3	1431	4	US-09-540-236-486	Sequence 486, App
	15	244.2	17.0	65792	4	US-09-596-002-31	Sequence 31, Appl
c	16	170.8	11.9	1664976	4	US-08-916-421B-1	Sequence 1, Appli
c	17	170.8	11.9	1664976	4	US-09-692-570-1	Sequence 1, Appli
	18	150	10.5	1341	3	US-08-724-814-19	Sequence 19, Appl
c	19	148.4	10.3	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	20	148.4	10.3	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	21	138.8	9.7	2664	4	US-09-902-540-8810	Sequence 8810, Ap
	22	138.8	9.7	8122	4	US-09-902-540-937	Sequence 937, App
	23	133.8	9.3	1341	4	US-09-710-279-2249	Sequence 2249, Ap
	24	133.8	9.3	1359	3	US-09-134-001C-1336	Sequence 1336, Ap
	25	133.8	9.3	3666	4	US-09-710-279-3543	Sequence 3543, Ap
	26	133.8	9.3	3861	4	US-09-710-279-4124	Sequence 4124, Ap
	27	130.2	9.1	447	4	US-09-252-991A-16138	Sequence 16138, A
	28	126	8.8	1347	4	US-09-583-110-2001	Sequence 2001, Ap
c	29	126	8.8	13425	3	US-08-961-527-151	Sequence 151, App
	30	125.2	8.7	4259	3	US-09-155-183-12	Sequence 12, Appl
	31	125.2	8.7	4259	4	US-09-733-383-12	Sequence 12, Appl
c	32	124.2	8.7	1425	4	US-09-252-991A-10987	Sequence 10987, A
	33	124.2	8.7	1470	4	US-09-252-991A-11262	Sequence 11262, A
	34	116.6	8.1	1350	4	US-09-252-991A-1330	Sequence 1330, Ap
	35	116.6	8.1	2538	4	US-09-252-991A-1285	Sequence 1285, Ap
c	36	116.6	8.1	2571	4	US-09-252-991A-1279	Sequence 1279, Ap
	37	114.6	8.0	576	4	US-09-252-991A-11196	Sequence 11196, A
	38	97.6	6.8	1347	4	US-09-252-991A-10926	Sequence 10926, A
	39	97.6	6.8	1395	4	US-09-252-991A-10988	Sequence 10988, A
	40	92.2	6.4	726	4	US-09-134-000C-1562	Sequence 1562, Ap
	41	91.4	6.4	1269	4	US-09-902-540-2402	Sequence 2402, Ap
	42	91.4	6.4	16782	4	US-09-902-540-1105	Sequence 1105, Ap
	43	89.6	6.2	1359	4	US-09-252-991A-11454	Sequence 11454, A
	44	89.6	6.2	1395	4	US-09-252-991A-11477	Sequence 11477, A
c	45	89.6	6.2	1452	4	US-09-252-991A-11417	Sequence 11417, A

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 23, 2005, 18:14:46 ; Search time 987 Seconds
(without alignments)
9217.496 Million cell updates/sec

Title: US-10-790-224A-19
Perfect score: 1434
Sequence: 1 gtggcgtttgaaaccccgga.....aattgtacttcgactgctaa 1434

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7173243 seqs, 3172129809 residues

Total number of hits satisfying chosen parameters: 14346486

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1434	100.0	1434	21	US-10-790-224A-19	Sequence 19, Appl
2	1434	100.0	2500	19	US-10-720-177-3	Sequence 3, Appli
3	1424.4	99.3	3309400	9	US-09-738-626-1	Sequence 1, Appli
4	1421.4	99.1	1431	9	US-09-738-626-3485	Sequence 3485, Ap
5	933.2	65.1	1434	17	US-10-282-122A-17591	Sequence 17591, A
6	705.8	49.2	1437	20	US-10-695-155-93	Sequence 93, Appl
7	705.8	49.2	38110	20	US-10-475-024-24	Sequence 24, Appl
8	705.8	49.2	38110	22	US-10-475-026-24	Sequence 24, Appl
9	693.2	48.3	2256646	19	US-10-470-565-1	Sequence 1, Appli
c 10	663.2	46.2	9025608	15	US-10-156-761-1	Sequence 1, Appli
11	660.4	46.1	1407	15	US-10-156-761-5982	Sequence 5982, Ap
12	483.8	33.7	1410	9	US-09-815-242-7990	Sequence 7990, Ap
13	483.8	33.7	1410	17	US-10-282-122A-30603	Sequence 30603, A
14	460.2	32.1	1497	17	US-10-282-122A-15130	Sequence 15130, A
15	458.8	32.0	1404	17	US-10-282-122A-31763	Sequence 31763, A
16	456	31.8	1413	17	US-10-282-122A-11289	Sequence 11289, A
17	449.6	31.4	1413	17	US-10-282-122A-13799	Sequence 13799, A
18	446.2	31.1	1407	17	US-10-282-122A-19817	Sequence 19817, A
c 19	440.8	30.7	1017	22	US-10-755-415-117	Sequence 117, App
20	434.8	30.3	1404	17	US-10-282-122A-33381	Sequence 33381, A
21	423.6	29.5	1410	17	US-10-282-122A-41379	Sequence 41379, A
22	419	29.2	1407	17	US-10-282-122A-23289	Sequence 23289, A
23	398	27.8	1410	17	US-10-282-122A-41832	Sequence 41832, A
24	392	27.3	1344	17	US-10-282-122A-13000	Sequence 13000, A
25	391.8	27.3	1410	9	US-09-815-242-6321	Sequence 6321, Ap
26	391.8	27.3	1410	15	US-10-299-799-2	Sequence 2, Appli
27	391.8	27.3	1410	17	US-10-282-122A-20584	Sequence 20584, A
28	391.8	27.3	1410	18	US-10-612-779-88	Sequence 88, Appl
29	391.2	27.3	1410	9	US-09-815-242-9691	Sequence 9691, Ap
30	391.2	27.3	1410	17	US-10-282-122A-39876	Sequence 39876, A
31	382.2	26.7	1419	17	US-10-282-122A-29891	Sequence 29891, A
32	375	26.2	1409	17	US-10-282-122A-37301	Sequence 37301, A
33	374.8	26.1	1533	17	US-10-282-122A-28986	Sequence 28986, A
34	338.2	23.6	1413	17	US-10-282-122A-8418	Sequence 8418, Ap
35	336.8	23.5	2731748	19	US-10-297-465A-1	Sequence 1, Appli
36	292.2	20.4	1407	17	US-10-282-122A-32655	Sequence 32655, A
37	286.4	20.0	1419	17	US-10-282-122A-31024	Sequence 31024, A
38	277.6	19.4	1419	9	US-09-815-242-7040	Sequence 7040, Ap
39	277.6	19.4	1419	17	US-10-282-122A-22148	Sequence 22148, A
40	277.6	19.4	1830121	17	US-10-329-670-1	Sequence 1, Appli
41	277.6	19.4	1830121	20	US-10-158-865-1	Sequence 1, Appli
42	277.6	19.4	1830121	22	US-10-981-687-1	Sequence 1, Appli
43	277.2	19.3	1407	17	US-10-282-122A-25145	Sequence 25145, A
44	244.2	17.0	1407	17	US-10-282-122A-26893	Sequence 26893, A
45	244.2	17.0	65792	18	US-10-672-787-31	Sequence 31, Appl

OM nucleic - nucleic search, using sw model

Run on: July 23, 2005, 11:32:21 ; Search time 5114 Seconds
 (without alignments)
 10673.477 Million cell updates/sec

Title: US-10-790-224A-19
 Perfect score: 1434
 Sequence: 1 gtggcggtttgaaaccccgga.....aattgtacttcgactgctaa 1434

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST:*
 1: gb_est1:*
 2: gb_est2:*
 3: gb_hlc:*
 4: gb_est3:*
 5: gb_est4:*
 6: gb_est5:*
 7: gb_est6:*
 8: gb_gss1:*
 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	246.6	17.2	1188	9	CG745336	CG745336 P038-1-H0
2	243.4	17.0	1069	8	BZ548371	BZ548371 pacs1-60_
c 3	191.2	13.3	840	9	CG146861	CG146861 PUIME33TD
c 4	176	12.3	478	1	AL587125	AL587125 AL587125
c 5	166	11.6	762	9	CG128373	CG128373 PUIFH05TD
c 6	166	11.6	851	8	CC381873	CC381873 PUHFA22TD
c 7	164	11.4	814	9	CL683966	CL683966 PRI0138b_
c 8	161.6	11.3	825	8	CC443184	CC443184 PUHFO69TD
c 9	161.6	11.3	850	8	BZ701245	BZ701245 PUBMN15TD

	10	159	11.1	488	7	CF606601	CF606601	FOGLI02_0
c	11	157.6	11.0	863	8	BZ574029	BZ574029	msh2_3475
	12	151.4	10.6	598	9	CG126167	CG126167	PUIFQ05TB
c	13	149.4	10.4	1236	8	BZ555775	BZ555775	pacs1-60_
c	14	144.6	10.1	1354	8	BZ548975	BZ548975	pacs1-60_
	15	143.4	10.0	883	8	CC439227	CC439227	PUHMO46TB
c	16	141.6	9.9	815	8	BZ705035	BZ705035	PUBMO84TD
	17	138.4	9.7	567	7	CF943093	CF943093	NcESTqab9
c	18	137.8	9.6	699	8	BZ684738	BZ684738	PUBFS60TD
c	19	130.2	9.1	799	9	CG110558	CG110558	PUIIA51TD
c	20	130.2	9.1	844	9	CG128001	CG128001	PUILH94TD
c	21	130.2	9.1	850	8	BZ704494	BZ704494	PUBMJ14TD
	22	130.2	9.1	901	8	CC435159	CC435159	PUHDF85TB
c	23	130.2	9.1	902	8	CC435165	CC435165	PUHDF85TD
c	24	130.2	9.1	944	8	BZ679052	BZ679052	PUBGZ43TD
c	25	130.2	9.1	1017	9	CG130318	CG130318	PUIFB78TD
	26	130	9.1	525	9	TSP458769	AJ458769	Thermotog
	27	123.4	8.6	320	6	CB821337	CB821337	EST 2188
	28	120.2	8.4	726	9	CG137357	CG137357	PUIHH87TB
	29	120.2	8.4	1138	2	BE636680	BE636680	rockefell
	30	117.2	8.2	910	8	CC381870	CC381870	PUHFA22TB
c	31	115.2	8.0	422	9	CG458779	CG458779	PUILB34TD
c	32	110.2	7.7	533	8	BZ296095	BZ296095	CG1855.f1
c	33	106.6	7.4	682	8	BZ668122	BZ668122	PUBCR86TD
c	34	106	7.4	954	8	BZ668332	BZ668332	PUBEZ18TD
c	35	102.8	7.2	382	9	CG107402	CG107402	PUILV62TD
	36	101.4	7.1	502	4	BM176045	BM176045	TgESTzyb2
	37	100.2	7.0	818	8	BZ687214	BZ687214	PUBDI18TD
c	38	96.8	6.8	481	8	AZ049103	AZ049103	GSSBru050
	39	96	6.7	540	8	BZ894864	BZ894864	Hg4_0154
c	40	91.6	6.4	786	8	CC377190	CC377190	PUHKI89TD
c	41	91.6	6.4	932	9	CG455027	CG455027	PUIJY83TD
c	42	89.4	6.2	1176	8	BZ569521	BZ569521	pacs2-164
	43	87.6	6.1	535	1	AL921359	AL921359	AL921359
c	44	78.2	5.5	1124	8	BZ558114	BZ558114	pacs1-60_
	45	77	5.4	255	8	BZ705385	BZ705385	PUBMJ94TD